

## **WHAT IS CLAIMED IS:**

1. An isolated nucleic acid molecule, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement and comprises a nucleic acid sequence selected from the group consisting of:
  - (a) a nucleic acid sequence which is a plant retroelement primer binding site and which has more than 95% identity to SEQ ID NO 2, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which is at least a portion of a plant retroelement envelope sequence and which has more than 50% identity to SEQ ID NO 5, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (c) a nucleic acid sequence which is at least a portion of a plant retroelement gag sequence and which has more than 50% identity to SEQ ID NO 7, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (d) a nucleic acid sequence which is at least a portion of a plant retroelement integrase sequence and which has more than 70% identity to SEQ ID NO 9, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (e) a nucleic acid sequence which is at least a portion of a plant retroelement reverse transcriptase sequence and which has more than 70% identity to SEQ ID NO 11, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (f) a nucleic acid sequence which is at least a portion of a plant retroelement protease sequence and which has more than 50% identity to SEQ ID NO 13, wherein said identity can be determined

using the DNAsis computer program and default parameters;

(g) a nucleic acid sequence which is at least a portion of a plant retroelement RNaseH sequence and which has more than 70% identity to SEQ ID NO 15, wherein said identity can be determined using the DNAsis computer program and default parameters;

(h) a nucleic acid sequence which is at least a portion of a plant retroelement sequence and which has more than 50% identity to SEQ ID NO 17, wherein said identity can be determined using the DNAsis computer program and default parameters;

(i) a nucleic acid sequence which is selected from the group consisting of: SEQ ID NO 2; SEQ ID NO 5; SEQ ID NO 7; SEQ ID NO 9; SEQ ID NO 11; SEQ ID NO 13; SEQ ID NO 15; and SEQ ID NO 17.

(j) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement envelope sequence and has more than 30% identity to SEQ ID NO 6, wherein said identity can be determined using the DNAsis computer program and default parameters;

(k) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement gag sequence and has more than 30% identity to SEQ ID NO 8, wherein said identity can be determined using the DNAsis computer program and default parameters;

(l) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement integrase sequence and has more than 75% identity to SEQ ID NO 10, wherein said identity can be determined using the DNAsis computer program and default parameters;

(m) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement reverse transcriptase sequence and has more than 79% identity to SEQ ID NO 12, wherein said identity can be determined using the DNAsis computer program and default parameters;

(n) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement protease sequence and has more than 55% identity to SEQ ID NO 14, wherein said identity can be determined using the DNAsis computer program and default parameters;

(o) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement RNaseH sequence and has more than 90% identity to SEQ ID NO 16, wherein said identity can be determined using the DNAsis computer program and default parameters;

(p) a nucleic acid sequence which encodes an amino acid sequence which is at least a portion of a plant retroelement sequence and has more than 40% identity to SEQ ID NO 18, wherein said identity can be determined using the DNAsis computer program;

(q) a nucleic acid sequence which encodes an amino acid sequence selected from the group consisting of: SEQ ID NO 4; SEQ ID NO 6; SEQ ID NO 8; SEQ ID NO 10; SEQ ID NO 12; SEQ ID NO 14; SEQ ID NO 16; and SEQ ID NO 18;

(r) a nucleic acid sequence which encodes an allelic variant of an amino acid sequence selected from the group consisting of: SEQ ID NO 4; SEQ ID NO 6; SEQ ID NO 8; SEQ ID NO 10; SEQ ID NO 12; SEQ ID NO 14; SEQ ID NO 16; and SEQ ID NO 18; and

(s) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); a nucleic acid sequence of (d); a nucleic acid sequence of (e); a nucleic acid sequence of (f); a nucleic acid sequence of (g); a nucleic acid sequence of (h); a nucleic acid sequence of (i); a nucleic acid sequence of (j); a nucleic acid sequence of (k); a nucleic acid sequence of (l); a nucleic acid sequence of (m); a nucleic acid sequence of (n); a nucleic acid sequence of (o); a nucleic acid sequence of (p); a nucleic acid sequence of (q); and a nucleic acid sequence of (r).

2. A seed comprising a nucleic acid of claim 1.
3. A plant comprising a nucleic acid of claim 1.
4. A nucleic acid molecule of 1, which comprises gag, pol and env genes and which comprises adenine-thymidine-guanidine as the gag gene start codon.
5. A nucleic acid molecule of claim 2, which further comprises SEQ ID NO 4.
6. An isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes at least a portion of a plant envelope sequence and comprises a nucleic acid sequence selected from the group consisting of:
  - (a) a nucleic acid sequence which has more than 90% identity to SEQ ID NO 5, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which encodes SEQ ID NO 5;

(c) a nucleic acid sequence which encodes an amino acid sequence which has greater than 85% identity to SEQ ID NO 6, wherein said identity can be determined using the DNAsis computer program and default parameters;

(d) a nucleic acid sequence which encodes amino acid sequence SEQ ID NO 6;

(e) a nucleic acid sequence which encodes an allelic variant of SEQ ID NO 6; and

(f) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); a nucleic acid sequence of (d); and a nucleic acid sequence of (e).

7. A plant cell comprising an isolated nucleic acid molecule of claim 6.
8. A plant retroviral envelope protein comprising an amino acid sequence encoded by a nucleic acid molecule of claim 6.
9. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a plant retroviral envelope protein of claim 8 to at least one plant cell under conditions sufficient to allow a nucleic acid molecule to enter said cell, wherein said nucleic acid molecule encodes an agronomically-significant characteristic.

10. An isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes at least a portion of a plant integrase sequence and comprises a nucleic acid sequence selected from the group consisting of:
- (a) a nucleic acid sequence which has more than 90% identity to SEQ ID NO 9, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which encodes SEQ ID NO 9;
  - (c) a nucleic acid sequence which encodes an amino acid sequence which has greater than 85% identity to SEQ ID NO 10, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (d) a nucleic acid sequence which encodes amino acid sequence SEQ ID NO 10;
  - (e) a nucleic acid sequence which encodes an allelic variant of SEQ ID NO 10; and
  - (f) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); a nucleic acid sequence of (d); and a nucleic acid sequence of (e).
11. A plant cell comprising an isolated nucleic acid molecule of claim 10.
12. A plant retroviral integrase protein comprising an amino acid sequence encoded by a compound of claim 10.

13. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a plant retroviral integrase protein of claim 12 to at least one plant cell under conditions sufficient to allow a nucleic acid molecule to enter said cell, wherein said nucleic acid molecule encodes an agronomically-significant characteristic.

14. An isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes at least a portion of a plant reverse transcriptase sequence and comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence which has more than 90% identity to SEQ ID NO 11, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid sequence which encodes SEQ ID NO 11;

(c) a nucleic acid sequence which encodes an amino acid sequence which has greater than 85% identity to SEQ ID NO 12, wherein said identity can be determined using the DNAsis computer program and default parameters;

(d) a nucleic acid sequence which encodes amino acid sequence SEQ ID NO 12;

(e) a nucleic acid sequence which encodes an allelic variant of SEQ ID NO 12; and

(f) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); a nucleic acid sequence of (d); and a nucleic acid sequence of (e).

15. A plant cell comprising an isolated nucleic acid molecule of claim 14.
16. A plant retroviral reverse transcriptase protein comprising an amino acid sequence encoded by a compound of claim 14.
17. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a plant retroviral reverse transcriptase protein of claim 16 to at least one plant cell under conditions sufficient to allow a nucleic acid molecule to enter said cell, wherein said nucleic acid molecule encodes an agronomically-significant characteristic.

18. An isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes at least a portion of a plant RNaseH sequence and comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence which has more than 90% identity to SEQ ID NO 15, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid sequence which encodes SEQ ID NO 15;

(c) a nucleic acid sequence which encodes an amino acid sequence which has greater than 95% identity to SEQ ID NO 16, wherein said identity can be determined using the DNAsis computer program and default parameters;

(d) a nucleic acid sequence which encodes amino acid sequence SEQ ID NO 16;

(e) a nucleic acid sequence which encodes an allelic variant of SEQ ID NO 16; and



- (f) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); a nucleic acid sequence of (d); and a nucleic acid sequence of (e).
19. A plant cell comprising an isolated nucleic acid molecule of claim 18.
20. A plant retroviral RNaseH protein comprising an amino acid sequence encoded by a compound of claim 18.
21. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:
- contacting a plant retroviral RNaseH protein of claim 18 to at least one plant cell under conditions sufficient to allow a nucleic acid molecule to enter said cell, wherein said nucleic acid molecule encodes an agronomically-significant characteristic.
22. An isolated retroelement comprising a nucleic acid sequence selected from the group consisting of:
- (a) a nucleic acid sequence which has more than 95% identity to SEQ ID NO 2; wherein said identity can be determined using the DNAsis computer program and default parameters;
- (b) a nucleic acid sequence which is SEQ ID NO 2;
- (c) a nucleic acid sequence which encodes amino acid sequence SEQ ID NO 4; and
- (d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); and a nucleic acid sequence of (c).

23. A plant retroelement of claim 22, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.
24. A plant retroelement of claim 23, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance; improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.
25. A plant retroviral particle of claim 23, wherein the agronomically significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.
26. An isolated plant retroviral particle comprising an isolated retroelement of claim 22.
27. A seed comprising comprising a plant retroelement of claim 22.
28. A plant comprising a plant retroelement of claim 22.
29. A plant of claim 28, which plant is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; cabbage; oat; rye; cotton; flax; potato; pine; walnut; citrus (including oranges, grapefruit etc.); hemp; oak; rice; petunia; orchids; Arabidopsis; broccoli; cauliflower; brussel sprouts; onion; garlic; leek; squash; pumpkin; celery; pea; bean (including various legumes); strawberries; grapes; apples; pears; peaches; banana; palm; cocoa; cucumber; pineapple; apricot; plum; sugar beet; lawn grasses; maple; triticale; safflower; peanut; and olive.

30. A plant of claim 29, which is soybean.
31. A method to transfer nucleic acid into a plant cell, comprising contacting a plant retroelement of claim 22 with at least one plant cell under conditions sufficient to allow said plant retroelement to enter said cell.
32. A method to impart agronomically-significant characteristics to a plant, comprising contacting a plant retroelement of claim 23 with at least one plant cell under conditions sufficient to allow said plant retroelement to enter said cell.
33. A method of claim 32, wherein the plant retroelement is contacted with said cell via a plant retroviral particle of claim 34.
34. A plant retroviral particle comprising a plant-derived retrovirus envelope protein.
35. A plant retroviral particle of claim 34, which further comprises a plant retroviral protein selected from the group consisting of: plant-derived integrase; plant derived reverse transcriptase; plant-derived gag; and plant-derived RNaseH.
36. An isolated plant retroviral particle comprising a plant retroviral protein encoded by a nucleic acid sequence selected from the group consisting of:
  - (a) a nucleic acid sequence comprising (i) a nucleic acid sequence which encodes at least one plant retroviral envelope protein, and (ii) a nucleic acid sequence which has more than 60% identity to a nucleic acid sequence selected from the group consisting of: SEQ ID NO 9; SEQ ID NO 11; SEQ ID NO 15; SEQ ID NO 26; SEQ ID NO 27; SEQ ID NO 28; SEQ ID NO 29; SEQ ID NO 30; and SEQ ID NO 31, wherein said identity can be determined using the DNAsis computer program and default parameters;

- (b) a nucleic acid sequence which encodes an amino acid sequence encoded by a nucleic acid sequence (a);
  - (c) a nucleic acid sequence which encodes an allelic variant of an amino acid sequence encoded by a nucleic acid sequence of (a); and
  - (d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); and a nucleic acid sequence of (c).
37. A plant retroelement of claim 36, wherein said nucleic acid sequence as described in (a) comprises a nucleic acid sequence of claim 6.
38. A plant retroelement of claim 38, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.
39. An isolated retroviral particle comprising a plant retroviral protein encoded by a nucleic acid sequence selected from the group consisting of:
- (a) a nucleic acid sequence which has more than 80% identity to a nucleic acid sequence selected from the group consisting of: SEQ ID NO 9; SEQ ID NO 11; and SEQ ID NO 15, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which encodes a nucleic acid selected from the group consisting of: SEQ ID NO 9; SEQ ID NO 11; and SEQ ID NO 15;
  - (c) a nucleic acid sequence which encodes an amino acid sequence encoded by a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); and a nucleic acid sequence of (b);

(d) a nucleic acid sequence which encodes an allelic variant of an amino acid sequence encoded by a nucleic acid selected from the group consisting of: a nucleic acid sequence of (a); and a nucleic acid sequence of (b); and

(e) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); a nucleic acid sequence of (c); and a nucleic acid sequence of (d).

40. A plant retroviral particle of claim 39, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.
41. A plant retroviral particle of claim 40, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance; improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.
42. A plant retroviral particle of claim 40, wherein the agronomically significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.
43. A method to transfer nucleic acid into a plant cell, comprising contacting a plant retroviral particle of claim 39 to at least one plant cell under conditions sufficient to allow said nucleic acid to enter said cell.

44. A method to impart agronomically-significant characteristics to a plant, comprising contacting a plant retroviral particle of claim 40 to at least one plant cell under conditions sufficient to allow said nucleic acid to enter said cell.
45. A method to transfer nucleic acid into a plant cell, comprising contacting a plant retroviral particle of claim 36 to at least one plant cell under conditions sufficient to allow said nucleic acid to enter said cell.
46. A method to transfer nucleic acid into a plant cell, comprising contacting a plant retroviral particle of claim 37 to at least one plant cell under conditions sufficient to allow said nucleic acid to enter said cell.
47. A method to impart agronomically-significant characteristics to a plant, comprising contacting a plant retroviral particle of claim 38 to at least one plant cell under conditions sufficient to allow said nucleic acid to enter said cell.
48. An isolated nucleic acid having at least 20 contiguous nucleotides of the sequence shown in SEQ ID NO 17.